

<!--StartFragment-->RESULT 3

S51398

hypothetical protein YLR260w - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: hypothetical protein L8479.7

C;Species: *Saccharomyces cerevisiae*

C;Date: 05-May-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004

C;Accession: S51398

R;Miller, N.

submitted to the EMBL Data Library, November 1994

A;Description: The sequence of *S. cerevisiae* cosmid 8479.

A;Reference number: S51395

A;Accession: S51398

A;Molecule type: DNA

A;Residues: 1-687 <MIL>

A;Cross-references: UNIPROT:Q06147; UNIPARC:UPI000006977B; EMBL:U17244; NID:g577171; PIDN:

AAB67377.1; PID:g577178; GSPDB:GN00012; MIPS:YLR260w

C;Genetics:

A;Gene: SGD:LCB5; MIPS:YLR260w

A;Cross-references: SGD:S0004250

A;Map position: 12R

Query Match 18.5%; Score 356.5; DB 2; Length 687;
 Best Local Similarity 24.9%; Pred. No. 5.6e-24;
 Matches 102; Conservative 76; Mismatches 150; Indels 81; Gaps 11;

Qy 1 VLVLLNPRGGK GKALQLFRSHVQPLLAEEISFTLMLTERRNHARELVRSEELGRWDALV 60
 : |::|| ||||| :|| : :||| : | :: |: || |: | :: ::| :

Db 271 IFVIINPFGGK GKAKKLFMTKAKPLLLASRCSIEVVYTKYPGHAIEIAREMDIDKYDTIA 330

Qy 61 VM SGDGLMHEVVNGLMERPDWETAIQK-PLCSLPAGSGNALAASLNHYAGYEQVTNEDLL 119
 ||||: |||:||| :||| | : :| |||||:: | |: ||

Db 331 CASGDGIPHEVINGLYQRPDHSVKA FN NIAITEIPCGSGNAMSVC-HW-----TNNP-- 381

Qy 120 TNCTLLLCRRLLSPMNL LSLHTASGLR---LFSVLSLAWGFIADV DLESEKYRRLGEMRF 176
 : || | : : : ::|: | | | || :| ||: |: :| | :| ||

Db 382 SYSTLCLIKSIETRIDL M CCSQPSYAREHPKLSFLSQTYGLIAETDINTEFIRWMGPARF 441

Qy 177 TLGTFLRLAALRTY-----RGRLAYLPV----- 199
 || : : | :| | : :

Db 442 ELGVA FN I IQKKKYPCEIYVKYAAKSKNELKNHYLEHKNKGSLEFQHITMKNKDNE DCDNY 501

Qy 200 ---GRVGSKTPASPVVVQGPVDAHLV-----PLEEPVPSHWTV 235
 :: :||: ||:| :|| |

Db 502 NYENEYETENEDEDEDADADDED SH LISRD LADSSADQIKEEDFKIKYPLDEGIPSDWER 561

Qy 236 VPDEDFVLVLALLHS---HLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAME 291
 : | : | : : : : : | : | : | : : | : :

Db 562 L-DPNISNNLGIFYTGKMPYVAADTKFFPAALPSDGTMDMVITDARTSLTRMAPILLGLD 620

Qy 292 KGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHP 340
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Db 621 KGSHVLQ--PEVLH SKILAYKIIPKLG NGLFSVDGEKFPLEPLQVEIMP 667

<!--EndFragment-->